

# LPEseq\_manual.pdf

# **LPEseq manual**

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`generateData(n.gene=20000, n.cond=2, n.deg=0, eff=1000, n.rep=3, disp=0.25)`

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Generating simulation data

Arguments

n.gene: the number of genes (default 10 000)  
n.cond: the number of experimental conditions (default 2)  
n.deg: the number of differentially expressed genes (DEGs) (default 0)  
eff: count value difference of DEGs in counts  
n.rep: the number of replicates per each condition (default 1)  
disp: dispersion parameter, inverse of 'size' parameter for nbinom function (default 0.25)

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`LPEseq.normalise(data, method)`

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Normalising input data according to their total count values

Arguments

data: count value matrix (should not be count values)  
method: c("mean", "median") for summary of the column sums, default: "mean"

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`LPEseq.matrans(dat)`

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MA transformation of the data

Arguments

dat: expression data with non-replicate per each condition

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`LPEseq.outlier(dat, d)`

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Removing outlier

Arguments

dat: expression data with non-replicate per each condition  
d: expression difference between conditions

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`LPEseq.var(dat, n.bin, df, d)`

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Evaluating local pooled error variance with non-replicated data

Arguments

dat: expression data with non-replicate per each condition  
n.bin: the number of quantile bins  
df: degrees of freedom of smooth.spline() function  
d: expression difference of LPEseq.outlier() function

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`LPEseq.predict.var(gene_expr, spline.var)`

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Predicting variance per gene using LPEseq smoothing curve

Arguments

gene\_expr: gene expression whose variance to be estimated  
spline.var: output of LPEseq.var() function

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`LPEseq.test(expr1, expr2, n.bin=100, df=10, d=1)`

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Testing differential expression between two conditions

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expr1: a numeric vector or matrix in first condition  
expr2: a numeric vector or matrix in second condition  
n.bin: the number of quantile bins (default 100)  
df: degrees of freedom in smooth.spline() function (default 10)  
d: expression difference in LPEseq.outlier() function (default 1; use 2 for biological replicates)

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AVplot(dat, avg, w.value, logged=T)

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Plotting average intensity versus variance

Arguments:

dat: Expression data matrix  
avg: Measure for average value across the columns of the data matrix (default "mean")  
w.value: Parameter for lowess weight value (default 0.1)  
logged: Log transformed or not (default TRUE)